

#2



OIKE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/004,551

DATE: 01/28/2002

TIME: 16:42:53

Input Set : N:\Crif3\RULE60\10004551.raw

Output Set: N:\CRF3\01282002\J004551.raw

1 <110> APPLICANT: SHIMKETS, RICHARD A
 2 FERNANDES, ELMA
 3 <120> TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
 4 <130> FILE REFERENCE: 15966-559
 5 <140> CURRENT APPLICATION NUMBER: US/10/004,551
 C--> 6 <141> CURRENT FILING DATE: 2001-12-05
 7 <150> PRIOR APPLICATION NUMBER: 09/635,949
 8 <151> PRIOR FILING DATE: 2000-08-10
 9 <160> NUMBER OF SEQ ID NOS: 110
 10 <170> SOFTWARE: PatentIn Ver. 2.1
 11 <210> SEQ ID NO: 1
 12 <211> LENGTH: 1867
 13 <212> TYPE: DNA
 14 <213> ORGANISM: Homo sapiens
 15 <220> FEATURE:
 16 <221> NAME/KEY: CDS
 17 <222> LOCATION: (128)..(1828)
 18 <400> SEQUENCE: 1

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 21 gcccccgccc tccctgggtc cctcctctcc ctccccagta gacgctcgga caccagccgc 120
 22 ggcaagg atg gag ctg ggt tgc tgg acg cag ttg ggg ctc act ttt ctt 169
 23 Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu
 24 1 5 10
 25 cag ctc ctt ctc atc tcg tcc ttg cca aga gag tac aca gtc att aat 217
 26 Gln Leu Leu Leu Ile Ser Ser Leu Pro Arg Glu Tyr Thr Val Ile Asn
 27 15 20 25 30
 28 gaa gcc tgc cct gga gca gag tgg aat atc atg tgt cgg gag tgc tgt 265
 29 Glu Ala Cys Pro Gly Ala Glu Trp Asn Ile Met Cys Arg Glu Cys Cys
 30 35 40 45
 31 gaa tat gat cag att gag tgc gtc tgc ccc gga aag agg gaa gtc gtg 313
 32 Glu Tyr Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu Val Val
 33 50 55 60
 34 ggt tat acc atc cct tgc tgc agg aat gag gag aat gag tgt gac tcc 361
 35 Gly Tyr Thr Ile Pro Cys Cys Arg Asn Glu Glu Asn Glu Cys Asp Ser
 36 65 70 75
 37 tgc ctg atc cac cca ggt tgt acc atc ttt gaa aac tgc aag agc tgc 409
 38 Cys Leu Ile His Pro Gly Cys Thr Ile Phe Glu Asn Cys Lys Ser Cys
 39 80 85 90
 40 cga aat ggc tca tgg ggg ggt acc ttg gat gac ttc tat gtg aag ggg 457
 41 Arg Asn Gly Ser Trp Gly Gly Thr Leu Asp Asp Phe Tyr Val Lys Gly
 42 95 100 105 110
 43 ttc tac tgt gca gag tgc cga gca ggc tgg tac gga gga gac tgc atg 505
 44 Phe Tyr Cys Ala Glu Cys Arg Ala Gly Trp Tyr Gly Gly Asp Cys Met

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45		115		120		125	
46	cga tgt ggc cag gtt ctg	cga gcc cca aag ggt cag att ttg ttg gaa	553				
47	Arg Cys Gly Gln Val Leu Arg Ala Pro Lys Gly Gln Ile Leu Leu Glu						
48		130		135		140	
49	agc tat ccc cta aat gct cac tgt gaa tgg acc att cat gct aaa cct		601				
50	Ser Tyr Pro Leu Asn Ala His Cys Glu Trp Thr Ile His Ala Lys Pro						
51		145		150		155	
52	ggg ttt gtc atc caa cta aga ttt gtc atg ttg agc ctg gag ttt gac		649				
53	Gly Phe Val Ile Gln Leu Arg Phe Val Met Leu Ser Leu Glu Phe Asp						
54		160		165		170	
55	tac atg tgc cag tat gac tat gtt gag gtt cgt gat gga gac aac cgc		697				
56	Tyr Met Cys Gln Tyr Asp Tyr Val Glu Val Arg Asp Gly Asp Asn Arg						
57		175		180		185	
58	gat ggc cag atc atc aag cgt gtc tgt ggc aac gag cgg cca gct cct		745				
59	Asp Gly Gln Ile Ile Lys Arg Val Cys Gly Asn Glu Arg Pro Ala Pro						
60		195		200		205	
61	atc cag agc ata gga tcc tca ctc cac gtc ctc ttc cac tcc gat ggc		793				
62	Ile Gln Ser Ile Gly Ser Ser Leu His Val Leu Phe His Ser Asp Gly						
63		210		215		220	
64	tcc aag aat ttt gac ggt ttc cat gcc att tat gag gag atc aca gca		841				
65	Ser Lys Asn Phe Asp Gly Phe His Ala Ile Tyr Glu Glu Ile Thr Ala						
66		225		230		235	
67	tgc tcc tca tcc cct tgt ttc cat gac ggc acg tgc gtc ctt gac aag		889				
68	Cys Ser Ser Ser Pro Cys Phe His Asp Gly Thr Cys Val Leu Asp Lys						
69		240		245		250	
70	gct gga tct tac aag tgt gcc tgc ttg gca ggc tat act ggg cag cgc		937				
71	Ala Gly Ser Tyr Lys Cys Ala Cys Leu Ala Gly Tyr Thr Gly Gln Arg						
72		255		260		265	
73	tgt gaa aat ctc ctt gaa gaa aga aac tgc tca gac cct ggg ggc cca		985				
74	Cys Glu Asn Leu Leu Glu Glu Arg Asn Cys Ser Asp Pro Gly Gly Pro						
75		275		280		285	
76	gtc aat ggg tac cag aaa ata aca ggg ggc cct ggg ctt atc aac gga		1033				
77	Val Asn Gly Tyr Gln Lys Ile Thr Gly Gly Pro Gly Leu Ile Asn Gly						
78		290		295		300	
79	cgc cat gct aaa att ggc acc gtg gtg tct ttc ttt tgt aac aac tcc		1081				
80	Arg His Ala Lys Ile Gly Thr Val Val Ser Phe Phe Cys Asn Asn Ser						
81		305		310		315	
82	tat gtt ctt agt ggc aat gag aaa aga act tgc cag cag aat gga gag		1129				
83	Tyr Val Leu Ser Gly Asn Glu Lys Arg Thr Cys Gln Gln Asn Gly Glu						
84		320		325		330	
85	tgg tca ggg aaa cag ccc atc tgc ata aaa gcc tgc cga gaa cca aag		1177				
86	Trp Ser Gly Lys Gln Pro Ile Cys Ile Lys Ala Cys Arg Glu Pro Lys						
87		335		340		345	
88	att tca gac ctg gtg aga agg aga gtt ctt ccg atg cag gtt cag tca		1225				
89	Ile Ser Asp Leu Val Arg Arg Arg Val Leu Pro Met Gln Val Gln Ser						
90		355		360		365	
91	agg gag aca cca tta cac cag cta tac tca gcg gcc ttc agc aag cag		1273				
92	Arg Glu Thr Pro Leu His Gln Leu Tyr Ser Ala Ala Phe Ser Lys Gln						
93		370		375		380	

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94   aaa ctg cag agt gcc cct acc aag aag cca gcc ctt ccc ttt gga gat   1321
95   Lys Leu Gln Ser Ala Pro Thr Lys Lys Pro Ala Leu Pro Phe Gly Asp
96       385                               390                               395
97   ctg ccc atg gga tac caa cat ctg cat acc cag ctc cag tat gag tgc   1369
98   Leu Pro Met Gly Tyr Gln His Leu His Thr Gln Leu Gln Tyr Glu Cys
99       400                               405                               410
100  atc tca ccc ttc tac cgc cgc ctg ggc agc agc agg agg aca tgt ctg   1417
101  Ile Ser Pro Phe Tyr Arg Arg Leu Gly Ser Ser Arg Arg Thr Cys Leu
102  415                               420                               425                               430
103  agg act ggg aag tgg agt ggg cgg gca cca tcc tgc atc cct atc tgc   1465
104  Arg Thr Gly Lys Trp Ser Gly Arg Ala Pro Ser Cys Ile Pro Ile Cys
105       435                               440                               445
106  ggg aaa att gag aac atc act gct cca aag acc caa ggg ttg tgg tgg   1513
107  Gly Lys Ile Glu Asn Ile Thr Ala Pro Lys Thr Gln Gly Leu Arg Trp
108       450                               455                               460
109  ccg tgg cag gca gcc atc tac agg agg acc agc ggg gtg cat gac ggc   1561
110  Pro Trp Gln Ala Ala Ile Tyr Arg Arg Thr Ser Gly Val His Asp Gly
111       465                               470                               475
112  agc cta cac aag gga gcg tgg ttc cta gtc tgc agc ggt gcc ctg gtg   1609
113  Ser Leu His Lys Gly Ala Trp Phe Leu Val Cys Ser Gly Ala Leu Val
114       480                               485                               490
115  aat gag cgc act gtg gtg gtg gct gcc cac tgt gtt act gac ctg ggg   1657
116  Asn Glu Arg Thr Val Val Val Ala Ala His Cys Val Thr Asp Leu Gly
117  495                               500                               505                               510
118  aag gtc acc atg atc aag aca gca gac ctg aaa gtt gtt ttg ggg aaa   1705
119  Lys Val Thr Met Ile Lys Thr Ala Asp Leu Lys Val Val Leu Gly Lys
120       515                               520                               525
121  ttc tac cgg gat gat gac cgg gat gag aag acc atc cag agc cta cag   1753
122  Phe Tyr Arg Asp Asp Asp Arg Asp Glu Lys Thr Ile Gln Ser Leu Gln
123       530                               535                               540
124  att tct gct atc att ctg cat ccc aac tat gac ccc atc ctt gct ttg   1801
125  Ile Ser Ala Ile Ile Leu His Pro Asn Tyr Asp Pro Ile Leu Ala Leu
126       545                               550                               555
127  atg ctt gac atc gcc atc ctg aac tcc tagacaaggc ccgtatcagc   1848
128  Met Leu Asp Ile Ala Ile Leu Asn Ser
129       560                               565
130  acccgagtcc agcccatct   1867
132 <210> SEQ ID NO: 2
133 <211> LENGTH: 567
134 <212> TYPE: PRT
135 <213> ORGANISM: Homo sapiens
136 <400> SEQUENCE: 2
137  Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln Leu
138      1                               5                               10                               15
139  Leu Leu Ile Ser Ser Leu Pro Arg Glu Tyr Thr Val Ile Asn Glu Ala
140      20                               25                               30
141  Cys Pro Gly Ala Glu Trp Asn Ile Met Cys Arg Glu Cys Cys Glu Tyr
142      35                               40                               45
143  Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu Val Val Gly Tyr

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144		50		55		60											
145	Thr	Ile	Pro	Cys	Cys	Arg	Asn	Glu	Glu	Asn	Glu	Cys	Asp	Ser	Cys	Leu	
146	65					70					75					80	
147	Ile	His	Pro	Gly	Cys	Thr	Ile	Phe	Glu	Asn	Cys	Lys	Ser	Cys	Arg	Asn	
148					85					90						95	
149	Gly	Ser	Trp	Gly	Gly	Thr	Leu	Asp	Asp	Phe	Tyr	Val	Lys	Gly	Phe	Tyr	
150				100					105					110			
151	Cys	Ala	Glu	Cys	Arg	Ala	Gly	Trp	Tyr	Gly	Gly	Asp	Cys	Met	Arg	Cys	
152				115				120					125				
153	Gly	Gln	Val	Leu	Arg	Ala	Pro	Lys	Gly	Gln	Ile	Leu	Leu	Glu	Ser	Tyr	
154	130						135					140					
155	Pro	Leu	Asn	Ala	His	Cys	Glu	Trp	Thr	Ile	His	Ala	Lys	Pro	Gly	Phe	
156	145					150					155					160	
157	Val	Ile	Gln	Leu	Arg	Phe	Val	Met	Leu	Ser	Leu	Glu	Phe	Asp	Tyr	Met	
158					165					170					175		
159	Cys	Gln	Tyr	Asp	Tyr	Val	Glu	Val	Arg	Asp	Gly	Asp	Asn	Arg	Asp	Gly	
160				180					185				190				
161	Gln	Ile	Ile	Lys	Arg	Val	Cys	Gly	Asn	Glu	Arg	Pro	Ala	Pro	Ile	Gln	
162				195				200				205					
163	Ser	Ile	Gly	Ser	Ser	Leu	His	Val	Leu	Phe	His	Ser	Asp	Gly	Ser	Lys	
164				210			215					220					
165	Asn	Phe	Asp	Gly	Phe	His	Ala	Ile	Tyr	Glu	Glu	Ile	Thr	Ala	Cys	Ser	
166	225					230					235					240	
167	Ser	Ser	Pro	Cys	Phe	His	Asp	Gly	Thr	Cys	Val	Leu	Asp	Lys	Ala	Gly	
168					245					250					255		
169	Ser	Tyr	Lys	Cys	Ala	Cys	Leu	Ala	Gly	Tyr	Thr	Gly	Gln	Arg	Cys	Glu	
170				260					265				270				
171	Asn	Leu	Leu	Glu	Glu	Arg	Asn	Cys	Ser	Asp	Pro	Gly	Gly	Pro	Val	Asn	
172				275				280				285					
173	Gly	Tyr	Gln	Lys	Ile	Thr	Gly	Gly	Pro	Gly	Leu	Ile	Asn	Gly	Arg	His	
174				290			295				300						
175	Ala	Lys	Ile	Gly	Thr	Val	Val	Ser	Phe	Phe	Cys	Asn	Asn	Ser	Tyr	Val	
176	305					310					315					320	
177	Leu	Ser	Gly	Asn	Glu	Lys	Arg	Thr	Cys	Gln	Gln	Asn	Gly	Glu	Trp	Ser	
178					325					330					335		
179	Gly	Lys	Gln	Pro	Ile	Cys	Ile	Lys	Ala	Cys	Arg	Glu	Pro	Lys	Ile	Ser	
180				340					345					350			
181	Asp	Leu	Val	Arg	Arg	Arg	Val	Leu	Pro	Met	Gln	Val	Gln	Ser	Arg	Glu	
182				355				360					365				
183	Thr	Pro	Leu	His	Gln	Leu	Tyr	Ser	Ala	Ala	Phe	Ser	Lys	Gln	Lys	Leu	
184				370			375					380					
185	Gln	Ser	Ala	Pro	Thr	Lys	Lys	Pro	Ala	Leu	Pro	Phe	Gly	Asp	Leu	Pro	
186	385					390					395					400	
187	Met	Gly	Tyr	Gln	His	Leu	His	Thr	Gln	Leu	Gln	Tyr	Glu	Cys	Ile	Ser	
188					405					410					415		
189	Pro	Phe	Tyr	Arg	Arg	Leu	Gly	Ser	Ser	Arg	Arg	Thr	Cys	Leu	Arg	Thr	
190				420					425					430			
191	Gly	Lys	Trp	Ser	Gly	Arg	Ala	Pro	Ser	Cys	Ile	Pro	Ile	Cys	Gly	Lys	
192				435				440					445				

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193   Ile Glu Asn Ile Thr Ala Pro Lys Thr Gln Gly Leu Arg Trp Pro Trp
194       450                               455                               460
195   Gln Ala Ala Ile Tyr Arg Arg Thr Ser Gly Val His Asp Gly Ser Leu
196       465                               470                               475                               480
197   His Lys Gly Ala Trp Phe Leu Val Cys Ser Gly Ala Leu Val Asn Glu
198       485                               490                               495
199   Arg Thr Val Val Val Ala Ala His Cys Val Thr Asp Leu Gly Lys Val
200       500                               505                               510
201   Thr Met Ile Lys Thr Ala Asp Leu Lys Val Val Leu Gly Lys Phe Tyr
202       515                               520                               525
203   Arg Asp Asp Asp Arg Asp Glu Lys Thr Ile Gln Ser Leu Gln Ile Ser
204       530                               535                               540
205   Ala Ile Ile Leu His Pro Asn Tyr Asp Pro Ile Leu Ala Leu Met Leu
206       545                               550                               555                               560
207   Asp Ile Ala Ile Leu Asn Ser
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210 <210> SEQ ID NO: 3
211 <211> LENGTH: 2306
212 <212> TYPE: DNA
213 <213> ORGANISM: Homo sapiens
214 <220> FEATURE:
215 <221> NAME/KEY: CDS
216 <222> LOCATION: (128)..(2287)
217 <400> SEQUENCE: 3
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219   gcccccggcc tccctgggtc cctcctctcc ctccccagta gacgctcgga caccagccgc 120
220   ggcaagg atg gag ctg ggt tgc tgg acg cag ttg ggg ctc act ttt ctt 169
221       Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu
222           1                               5                               10
223   cag ctc ctt ctc atc tgc tcc ttg cca aga gag tac aca gtc att aat 217
224   Gln Leu Leu Leu Ile Ser Ser Leu Pro Arg Glu Tyr Thr Val Ile Asn
225       15                               20                               25                               30
226   gaa gcc tgc cct gga gca gag tgg aat atc atg tgt cgg gag tgc tgt 265
227   Glu Ala Cys Pro Gly Ala Glu Trp Asn Ile Met Cys Arg Glu Cys Cys
228       35                               40                               45
229   gaa tat gat cag att gag tgc gtc tgc ccc gga aag agg gaa gtc gtg 313
230   Glu Tyr Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu Val Val
231       50                               55                               60
232   ggt tat acc atc cct tgc tgc agg aat gag gag aat gag tgt gac tcc 361
233   Gly Tyr Thr Ile Pro Cys Cys Arg Asn Glu Glu Asn Glu Cys Asp Ser
234       65                               70                               75
235   tgc ctg atc cac cca ggt tgt acc atc ttt gaa aac tgc aag agc tgc 409
236   Cys Leu Ile His Pro Gly Cys Thr Ile Phe Glu Asn Cys Lys Ser Cys
237       80                               85                               90
238   cga aat ggc tca tgg ggg ggt acc ttg gat gac ttc tat gtg aag ggg 457
239   Arg Asn Gly Ser Trp Gly Gly Thr Leu Asp Asp Phe Tyr Val Lys Gly
240       95                               100                               105                               110
241   ttc tac tgt gca gag tgc cga gca ggc tgg tac gga gga gac tgc atg 505
242   Phe Tyr Cys Ala Glu Cys Arg Ala Gly Trp Tyr Gly Gly Asp Cys Met

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VERIFICATION SUMMARY

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L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1500 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1853 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:2045 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:2424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27